

AMENDMENTS

IN THE CLAIMS:

1. (Withdrawn) A predefined pooled collection of distinct nucleic acid vectors, wherein each constituent member of said pooled collection comprises an expression cassette that corresponds to a chromosomal transcript of known sequence.
2. (Withdrawn) The pooled collection according to Claim 1, wherein said collection comprises at least 100 distinct nucleic acid vectors.
3. (Withdrawn) The pooled collection according to Claim 2, wherein said collection comprises at least 1000 distinct nucleic acid vectors.
4. (Withdrawn) The pooled collection according to Claim 1, wherein said pooled collection is a library of ESTs.
- 5-26. (Canceled)
27. (Currently Amended) A method comprising:
 - (a) dividing an initial set of a plurality of separate nucleic acids into at least two pooled collections of nucleic acids having an initial sequence representation profile, wherein each pooled collection includes not more than about 100 distinct nucleic acids;
 - (b) amplifying each of said pooled collections to produce ~~two or more~~ amplified pooled collections; and
 - (c) combining said ~~two or more~~ amplified pooled collections to produce a non-cellular nucleic acid library, wherein said non-cellular nucleic acid library is a collection of separate nucleic acids with a sequence representation profile that is substantially the same as said initial sequence representation profile.
28. (Original) The method according to Claim 27, wherein said non-cellular nucleic acid library is an EST library.
29. (Previously Presented) The method according to Claim 27, wherein said non-cellular nucleic acid library is a library containing sequences complementary to at least a segment of a chromosomal transcript.

30. (Previously Presented) The method according to Claim 27, wherein the nucleic acids of said non-cellular nucleic acid library are in vectors.

31. (Previously Presented) The method according to Claim 27, wherein said vectors are integrating vectors.

32. (Original) The method according to Claim 27, wherein said non-cellular nucleic acid library comprises a substantially equal amount of each constituent nucleic acid member.

33. (Original) The method according to Claim 27, wherein said non-cellular nucleic acid library has a ratio of number of different nucleic acids to total amount of nucleic acid that ranges from about 10/ μ g to about 10,000/ μ g.

34. (Previously Presented) The method according to Claim 33, wherein said non-cellular nucleic acid library comprises at least 1000 nucleic acids of different sequence.

35. (Withdrawn) A non-cellular nucleic acid library produced according to the method of Claim 27.

36. (Withdrawn) A cellular nucleic acid library produced by transforming a population of cells with a non-cellular library according to Claim 35.

37-44. (Canceled)

45. (Previously Presented) The method according to Claim 27, wherein each nucleic acid of said non-cellular nucleic acid library comprises an expression cassette that corresponds to a chromosomal transcript of known sequence.

46. (Previously Presented) The method according to Claim 27, wherein said non-cellular nucleic acid library is an antisense library.

47. (Previously Presented) The method according to Claim 27, wherein said non-cellular nucleic acid library is a sense library.
48. (Withdrawn) The method according to Claim 27, further comprising contacting a population of cells with said non-cellular nucleic acid library, wherein the expression of one or more chromosomal coding regions in said population of cells is reduced.
49. (Withdrawn) The method according to Claim 48, wherein said non-cellular nucleic acid library is an EST library.
50. (Withdrawn) The method according to Claim 48, wherein said non-cellular nucleic acid library is a library containing sequences complementary to at least a segment of a chromosomal transcript.
51. (Withdrawn) The method according to Claim 48, wherein the nucleic acids of said non-cellular nucleic acid library are in vectors.
52. (Withdrawn) The method according to Claim 48, wherein said vectors are integrating vectors.
53. (Withdrawn) The method according to Claim 48, wherein said non-cellular nucleic acid library comprises a substantially equal amount of each constituent nucleic acid member.
54. (Withdrawn) The method according to Claim 48, wherein said non-cellular nucleic acid library has a ratio of number of different nucleic acids to total amount of nucleic acid that ranges from about 10/ μ g to about 10,000/ μ g.
55. (Withdrawn) The method according to Claim 48, wherein said non-cellular nucleic acid library comprises at least 1000 nucleic acids of different sequence.
56. (Withdrawn) The method according to Claim 48, wherein each nucleic acid of said non-cellular nucleic acid library comprises an expression cassette that corresponds to a chromosomal transcript of known sequence.

57. (Withdrawn) The method according to Claim 48, wherein said non-cellular nucleic acid library is an antisense library.

58. (Withdrawn) The method according to Claim 48, wherein said non-cellular nucleic acid library is a sense library.

59. (Withdrawn) The method according to Claim 48, wherein said method is a method of identifying a genomic coding sequence of interest.

60. (Withdrawn) The method according to Claim 48, wherein said method is a method of determining function of a genomic coding sequence.

61. (Withdrawn) The method according to Claim 27, further comprising:
transforming a population of cells with said non-cellular nucleic acid library to produce a cellular library; and
identifying members of said cellular library that display a phenotype of interest to identify a genomic coding sequence of interest.

62. (Withdrawn) The method according to Claim 61, wherein said non-cellular nucleic acid library is an EST library.

63. (Withdrawn) The method according to Claim 61, wherein said non-cellular nucleic acid library is a library containing sequences complementary to at least a segment of a chromosomal transcript.

64. (Withdrawn) The method according to Claim 61, wherein the nucleic acids of said non-cellular nucleic acid library are in vectors.

65. (Withdrawn) The method according to Claim 61, wherein said vectors are integrating vectors.

66. (Withdrawn) The method according to Claim 61, wherein said non-cellular nucleic acid library comprises a substantially equal amount of each constituent nucleic acid member.

67. (Withdrawn) The method according to Claim 61, wherein said non-cellular nucleic acid library has a ratio of number of different nucleic acids to total amount of nucleic acid that ranges from about 10/ μ g to about 10,000/ μ g.

68. (Withdrawn) The method according to Claim 61, wherein said non-cellular nucleic acid library comprises at least 1000 nucleic acids of different sequence.

69. (Withdrawn) The method according to Claim 61, wherein each nucleic acid of said non-cellular nucleic acid library comprises an expression cassette that corresponds to a chromosomal transcript of known sequence.

70. (Withdrawn) The method according to Claim 61, wherein said non-cellular nucleic acid library is an antisense library.

71. (Withdrawn) The method according to Claim 61, wherein said non-cellular nucleic acid library is a sense library.

72. (Withdrawn) The method according to Claim 61, wherein said phenotype of interest results from loss of function of said genomic coding sequence of interest.

73. (Withdrawn) The method according to Claim 61, wherein the phenotype of interest is resistance to infection by a virus.

74. (Withdrawn) The method according to Claim 61, wherein the phenotype of interest is resistance to the pathogenicity of bacteria.